

EXHIBIT 1




Search **Nucleotide** for **Go** **Clear**

Limits **Preview/Index** **History** **Clipboard** **Details**

Display **GenBank(Full)** **Show 5** **Send to**

Range: from **3527982** to **3628476** **Show whole sequence** **Reverse complemented str.**

☐ **I: BA000043. Reports** **Geobacillus kaust...[gi:56378377]**

[Links](#)

Features **Sequence**

LOCUS BA000043 495 bp DNA linear BCT 04-DEC-2004
DEFINITION Geobacillus kaustophilus HTA426 DNA, complete genome.
ACCESSION BA000043 REGION: 3527982..3628476
VERSION BA000043.1 GI:56378377
KEYWORDS .
SOURCE Geobacillus kaustophilus HTA426
ORGANISM Geobacillus kaustophilus HTA426
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Geobacillus.

REFERENCE 1
AUTHORS Takami,H., Takaki,Y., Chee,G.J., Nishi,S., Shimamura,S., Suzuki,H., Matsui,S. and Uchiyama,I.
TITLE Thermoadaptation trait revealed by the genome sequence of thermophilic Geobacillus kaustophilus
JOURNAL (er) Nucleic Acids Res. 32 (21), 6292-6303 (2004)
PUBMED 15576355

REFERENCE 2 (bases 1 to 495)
AUTHORS Takami,H., Takaki,Y. and Chee,G.
TITLE Direct Submission
JOURNAL Submitted (25-JUN-2003) Hideto Takami, Japan Marine Science and Technology Center, Microbial Genome Analysis Research Group; 2-15 Natsushima-cho, Yokosuka, Kanagawa 237-0061, Japan
 (E-mail: takami@jamstec.go.jp,
 URL: http://www.jamstec.go.jp/jamstec-e/bio/exbase.html,
 Tel: 81-46-867-9643, Fax: 81-46-867-9645)

FEATURES
 source
 1..495
 /organism="Geobacillus kaustophilus HTA426"
 /mol_type="genomic DNA"
 /strain="HTA426"
 /isolation_source="isolated from the deepest Ocean"
 /db_xref="taxon:335009"
 /note="thermophile"

gene
 complement(1..495)
 /locus_tag="GK3481"

CDS
 complement(1..495)
 /locus_tag="GK3481"
 /codon_start=1
 /transl_table=11
 /product="single-strand DNA-binding protein"
 /protein_id="BAD77766.1"
 /db_xref="GI:56381858"
 /translation="MINRVILVGRLTROPETLPTSPGVAVATFTLAVNRPFTNQOGER
 ETDFIQCVVWRQAENVANFLKKGLAGVDGRLQTRSYENQEGRRVYVTEVADSVQF

LEPKGTSQKRGATAGCYYGDFFFQDQNHQ / PNEKGFGRIDDDPFANDQQPJDIDSD
DLFF"

ORIGIN

```

1  ttaaaaacggc aaatcatcat cagaaatatt gatgggtgg cagtcattgg cgaaggatc
61  gtcctcagatg cggccaaacc ctcttttcgtt cggatattgg tggttctgat cttgcccgaa
121 tgggaatgga tccccatagt agccgcttgc tgttgccctt cgttgctcgc tegtcccttt
181 cgggtcaaga aattggagcg tctcagccac cacttcctgt acgtacacgc gccgaccttc
241 ttgattctca tagctggggg tttagagtcg gccatcgaca ccagccaaag tcccttttt
301 cnaaaagttg gggacgtttt ccgcttggcg gccccaaacg accatttga taaaatccgt
361 ttcccgctcg cctgctgat ttgtaaacgg acggttgacc gccagcgtaa acgtggcaac
421 agccactcgg cttggagtggt aaagcaactc cggatctctc gttaacctgc ccgacaaaat
481 gacgcggcta atcat

```

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

Jul 24 2006 17:22:14



Search **Nucleotide** for **Go** **Clear**

Limits Preview/Index History Clipboard Details

Display **GenBank(Full)** Show **5** Send to **3**

Range: from **5398259** to **5398771** Show whole sequence ☐ Reverse complemented str.

I: AF016877. Reports **Bacillus cereus A...**[gi:29899096]

Links

Comment Features Sequence

LOCUS AF016877 513 bp DNA linear BCT 30-DEC-2005

DEFINITION *Bacillus cereus* ATCC 14579, complete genome.

ACCESSION AF016877 REGION: 5398259..5398771

VERSION AF016877.1 GI:29899096

KEYWORDS .

SOURCE *Bacillus cereus* ATCC 14579

ORGANISM *Bacillus cereus* ATCC 14579
Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*; *Bacillus cereus* group.

REFERENCE 1 (bases 1 to 513)

AUTHORS Ivanova,N., Sorokin,A., Anderson,I., Galleron,N., Candelon,B., Kapatal,V., Bhattacharyya,A., Reznik,G., Mikhailova,N., Lapidus,A., Chu,L., Mazur,M., Goltzman,E., Larsen,N., D'Souza,M., Walunas,T., Grechkin,Y., Fusch,G., Haselkorn,R., Fonstein,M., Ehrlich,D.S.D., Overbeek,R. and Kyrpides,N.

TITLE Genome sequence of *Bacillus cereus* and comparative analysis with *Bacillus anthracis*

JOURNAL Nature 423 (6935), 87-91 (2003)

PUBMED 12721630

REFERENCE 2 (bases 1 to 513)

AUTHORS Candelon,B., Gailloux,K., Ehrlich,D.S. and Sorokin,A.

TITLE The number of ribosomal RNA operons in *Bacillus cereus*

JOURNAL Unpublished

REFERENCE 3 (bases 1 to 513)

AUTHORS Ivanova,N., Sorokin,A., Anderson,I., Galleron,N., Candelon,B., Kapatal,V., Bhattacharyya,A., Reznik,G., Mikhailova,N., Lapidus,A., Chu,L., Mazur,M., Goltzman,E., Larsen,N., D'Souza,M., Walunas,T., Grechkin,Y., Fusch,G., Haselkorn,R., Fonstein,M., Ehrlich,D.S.D., Overbeek,R. and Kyrpides,N.

TITLE Direct Submission

JOURNAL Submitted (12-MAR-2003) INRA, Genetique Microbienne, Domaine de Vilvert, Jouy en Josas 78352, France

COMMENT On or before Dec 30, 2005 this sequence version replaced
gi:29899096, gi:29899097, gi:29899098, gi:29899099, gi:29899100, gi:29899101, gi:29899102, gi:29899103, gi:29899104, gi:29899105, gi:29899106, gi:29899107, gi:29899108, gi:29899109, gi:29899110, gi:29899111, gi:29899112, gi:29899113, gi:29899114, gi:29899115, gi:29899116, gi:29899117, gi:29899118, gi:29899119, gi:29899120, gi:29899121, gi:29899122, gi:29899123, gi:29899124.

FEATURES
source
1..513
/organism="Bacillus cereus ATCC 14579"
/mol_type="genomic DNA"
/strain="ATCC 14579"
/db_xref="ATCC:14579"





```

/db_xref="taxon:226900"
/focus
gene complement(1..513)
/locus_tag="BC_5475"
/old_locus_tag="BC5475"
CDS complement(1..513)
/locus_tag="BC_5475"
/old_locus_tag="BC5475"
/codon_start=1
/transl_table=11
/product="Single-strand DNA binding protein"
/protein_id="AAF12329.1"
/db_xref="GI:29899058"
/translation="MMNRVILVGRLLTKDPLRYTFNGVAVATFTLAVNRAFAAQQGER
EADPINCVMRKQAEENVANYLKKGLAGVDGRLQTRNYEGQDGKRVVYVFVLAESVQF
LEFRNGGGGQRGSFNQGSFGAGFGNQGSNPFQGSNSNCGNSGFTKNDFFSHVQGF
IDISDDDLFF"
ORIGIN
1 ttagaaacggt aaatogtctt cggaaatgtc gatcgggttga cctacatttg aaaatggatc
61 gtcattcttc gtaaatccag agttaacctg gttacctgaa ttactagatt gaccaaattg
121 gtttagagcct tggttaccga aaccagctcc tgatgggttg tgattaaatg aaccacgttg
181 ctccccacgg ccactaacgg gctctaaaaa ttgcacgctt ccgcaagaa cttctgttac
241 gtatcacagt ttaccatctt gtccctcgtg attacagatt tgaagacgac catctacgcc
301 tgctaaagct ccttttttca aataatttgc taagtcttct gcttggttac gccatattac
361 acaatttaata aagtcagatt cagctccacc ttgctgattg gcaaatgcgc gattccacgc
421 taacgtaaaa gtactctact cgaacacatt gggcgtgtaa cgtaagttag ggtccttagt
481 taaacgacca acgaggataa cagcattcat caa

```

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

Jul 24 2006 17:27:11

Nucleotide Protein Gene Structure PDB Taxonomy My NCBI
 [Sign In] [Register] [Bookmarks]

Search **Nucleotide** for **Go** **Clear**
 Limits Preview/Index History Clipboard Details

Display **GenBank(Full)** Show **5** Send to
 Range: from **554401** to **554931** Show whole sequence ☐ Reverse complemented str.

1: NZ_AAA02000001. Reports Bacillus anthracis...[gi:65316885]

[Links](#)

Comment Features Sequence

LOCUS NZ_AAA02000001 531 bp DNA linear BCT 16-MAY-2005

DEFINITION Bacillus anthracis str. A2012 Bant_02_1, whole genome shotgun sequence.

ACCESSION NZ_AAA02000001 REGION: 554401..554931

VERSION NZ_AAA02000001.1 GI:65316885

KEYWORDS WGS.

SOURCE Bacillus anthracis str. A2012

ORGANISM Bacillus anthracis str. A2012
Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group.

REFERENCE 1 (bases 1 to 531)

AUTHORS Read,T.D., Salzberg,S.L., Pop,M., Shumway,M., Umayam,L., Jiang,L., Holtzapple,E., Busch,J.D., Smith,K.L., Schupp,J.M., Solomon,D., Keim,P. and Fraser,C.M.

TITLE Comparative genome sequencing for discovery of novel polymorphisms in Bacillus anthracis

JOURNAL Science 296 (5575), 2028-2033 (2002)

PUBMED 12004073

REFERENCE 2 (bases 1 to 531)

AUTHORS NCBI Microbial Genomes Annotation Project.

TITLE Direct Submission

JOURNAL Submitted (16-MAY-2005) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA

COMMENT NOTE: Until 03/06/2003, this project code (NZ_AAA02000001) belonged to the GenBank version a change to the assembly-version number of the project, from 01 to 02, is necessitated.
Protein-coding genes were predicted using GeneMark and GeneMarkES programs (kindly provided by M. Borodovsky). Functional annotation is based on CDD (Conserved Domain Database) and COG (Clusters of Orthologous Groups) assignments, it has not yet been subject to manual review. DNA sequence and predicted proteins are available for BLAST at http://www.ncbi.nlm.nih.gov/sutils/genom_table.cgi.

FEATURES Location/Qualifiers

source 1..531
/organism="Bacillus anthracis str. A2012"
/mol_type="genomic DNA"
/strain="A2012"
/do_xref="taxon:191318"

gene complement(1..531)
/locus_tag="Bant_01000618"

CDS complement(1..531)
/locus_tag="Bant_01000618"

```

/codon_start=1
/product="COG0629: Single-stranded DNA-binding protein"
/protein_id="EF_00390413.1"
/db_xref="GI:65217454"
/db_xref="COG:COG0629"
/translation="MVRLMNRVILVGRLLTKDPDLRYTPNGVAVATFTLAVNRAFANQD
SEREADFLNCVIAWYQAENVANYLKKGSLAGVDORLQTRNYEGQGQKRVYVTEVLAES
YQFLEPRNGSGEQSGSFNQSGAGAGFNQSSNPFQSSNSGNGQNGSGFTKNDPF
SNVGQPIDISDDDLFF"

```

ORIGIN




```

1  ttagaacggt  aaatcgctgt  cggaaatgct  gatcgggtga  cctacatttg  aaantggatc
61  gtcatctctt  gtaaacccag  agttcccttg  gttacccctg  ttgcccgaat  tactagattg
121  accaaatggg  tttagagctt  ggttaacgaa  accagctcct  gatgggtgct  gattaaatga
181  accacgttgc  tcccccgcgc  catlaacggg  ctctaaaaat  tgtacgcttt  cggcaagaac
241  ttctgttaca  tatacaagct  taccatcttg  tccctcgtaa  ttacagagtt  gaagacgtcc
301  atctacgctt  gctaaagctc  ctctttttaa  ataatttgct  acgtttcttg  ctgttttagc
361  cctatttaca  caattaatca  agtcagcttc  acgtcacctt  tggtgattcg  cnaatgcggc
421  attcacagct  aacgtaaaa  tagctactgc  aacaccattg  ggctgttaac  gtaagtcagg
481  gtcccttagt  aaacgaccaa  cggagataac  acgattcctc  aatcgaaaca  c

```

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

Jul 21 2006 17:22:14

[PubMed](#) [Nucleotide](#) [Protein](#) [Genome](#) [Structure](#) [PMC](#) [Taxonomy](#) [GMM](#) [Books](#)

[Search Nucleotide](#) [for](#) [Go](#) [Clear](#)

[Limits](#) [Preview/Index](#) [History](#) [Clipboard](#) [Details](#)

[Display GenBank\(Full\)](#) [Show 5](#) [Send to](#)

Range: from 5224259 to 5224780 [Show whole sequence](#) ☐ [Reverse complemented str.](#)

☒ 1: AE017355. Reports *Bacillus thuringi...*[gi:49328240]

[Link](#)

[Comment](#) [Features](#) [Sequence](#)

LOCUS AE017355 522 bp DNA linear BCT 12-AUG-2004
DEFINITION *Bacillus thuringiensis* serovar konkukian str. 97-27, complete genome.
ACCESSION AE017355 REGION: 5224259..5224780
VERSION AE017355.1 GI:49328240
KEYWORDS .
SOURCE *Bacillus thuringiensis* serovar konkukian str. 97-27
ORGANISM *Bacillus thuringiensis* serovar konkukian str. 97-27
Bacteria; *Firmicutes*; *Bacillales*; *Bacillaceae*; *Bacillus*; *Bacillus cereus* group.
REFERENCE 1 (bases 1 to 522)
AUTHORS Brettin,T.S., Bruce,D., Challacombe,J.F., Gilna,P., Han,C., Hill,K., Hitchcock,P., Jackson,P., Keim,P., Longmire,J., Lucas,S., Okinaka,R., Richardson,P., Rubin,E. and Tice,H.
TITLE Complete genome sequence of *Bacillus thuringiensis* 97-27
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 522)
AUTHORS Brettin,T.S., Bruce,D., Challacombe,J.F., Gilna,P., Han,C., Hill,K., Hitchcock,P., Jackson,P., Keim,P., Longmire,J., Lucas,S., Okinaka,R., Richardson,P., Rubin,E. and Tice,H.
TITLE Direct Submission
JOURNAL Submitted (07-JUN-2004) Joint Genome Institute, Department of Energy, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT *Bacillus thuringiensis* 97-27 (subsp. konkukian (serotype H34)) was originally isolated from a case of severe human tissue necrosis (*Bacillus thuringiensis* subsp. konkukian (serotype H34) superinfection: Case report and experimental evidence of pathogenicity in immunosuppressed mice. Hernandez, E, Ramisse, F, Ducourau, J-P, Cruel, T, and Cavallo, J-D. J Clin Microbiol 1998 36(7):2138-2139). *B. thuringiensis* is indigenous to many habitats worldwide; these include soil, insects, deciduous and coniferous leaves (Prediction of insecticidal activity of *Bacillus thuringiensis* strains by polymerase chain reaction product profiles. Carozzi, NB, Kramer, VC, Warren, GW, Evola, S, and Koziel, MG. Appl Environ Microbiol. 1991 57(11):3057-61). *B. thuringiensis* is an insect pathogen that is widely used as a biopesticide in commercial agriculture. Infection of humans is unusual. The apparent pathogenic properties of *B. thuringiensis* 97-27 are very unusual for *B. thuringiensis*; unlike most *B. thuringiensis* isolates, this isolate is very closely related to *B. anthracis* based on phylogenetic analysis (Fluorescent amplified fragment length polymorphism analysis of *Bacillus anthracis*, *Bacillus cereus*, and *Bacillus thuringiensis* isolates. Hill, KK,

Ticknor, LO, Ckinaka, RT, Asay, M, Blair, H, Bliss, KA, Laker, M, Fardington, PE, Richardson, AF, Tonks, M, Beecher, DJ, Kemp, JD, Kolsto, A-B, Wong, ACL, Klein, P, and Jackson, PJ. Appl Environ Microbiol 70(12):1068-1080. Plasmid and fosmid libraries were prepared at the Joint Genome Institute in Los Alamos (JGI-LANL), NM. Shotgun sequencing was performed at the JGI Production Genomics Facility (JGI-PGF) in Walnut Creek, CA to a coverage of 24x. Finishing was performed at JGI-LANL starting with 83 contigs and 16 scaffolds. Repetitive regions were identified, assembled and finished by manually checking paired reads close to each repeat in the assembly with contigs and then making a subassembly for each repetitive region. Fifty five gaps were closed with primer walks and 16 by PCR. Gene predictions were obtained using Glimmer and tRNAs were identified using tRNAscan-SE. Basic analysis of the gene predictions was performed by comparing coding sequences against the Pfam, BLOCKS and Prodom databases. Gene definitions and functional classes were added manually by a team of annotators at JGI-LANL, using BLAST results in addition to information from the basic analysis. A total of 5540 features have been annotated on the sequence record.

```

FEATURES
    source                Location/Qualifiers
                        1..522
                        /organism="Bacillus thuringiensis serovar konkukian str.
                        97-27"
                        /mol_type="genomic DNA"
                        /strain="97-27"
                        /serovar="konkukian"
    gene                 /db_xref="taxon:281309"
                        complement(1..522)
                        /gene="ssb"
    CDS                   /locus_tag="BT9727_5154"
                        complement(1..522)
                        /gene="ssb"
                        /locus_tag="BT9727_5154"
                        /inference="non-experimental evidence, no additional
                        details recorded"
                        /codon_start=1
                        /transl_table=11
                        /product="single-stranded DNA-binding protein"
                        /protein_id="BAT62672.1"
                        /db_xref="GI:49332026"
                        /translation="MMNRVILVGRITKDPDLRYTPNGVAVATFTLAVNRAFAQQQER
                        EADFNCVIRKQAEVANYLLKKGSLAGVDGRLQTRNYEGQDGKRVYVTEVLAESVQF
                        LEPRNGGGEGQRGSFNQQPSGAGEGNQSNNPFGQSSNSGNQGNQNSGFTKNDFPFSNV
                        GQPIDISDDDLFF"

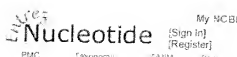
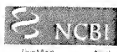
ORIGIN
    1 ttagaaacgtt aatogtgtt cggaaatgtc gatcgggtta cctacatttt aaaatggatc
    61 gtcatttcttc gtaaatccag agtttctctt gttacatttg ttgcocgaat tactagattg
    121 accaaattggg ttagagcttt ggttacgcaa accagctctc gatggttgct gattaatatga
    181 accacgtttgc tcocacccgc cactacgcgg cctataaaaat tgaacgtttt ccgcaagaac
    241 ttctgtttaca tatcacgcgt taccattctt tccctcgtta ttacagattt gaagaagctc
    301 atctacgcct gctaaagctac cttttttcaa ataatttgt acgtttttct ctgtttaag
    361 ccatattaca caattaataa agtcagcttc acgctcacct tgttgattgc caaatgcgcg
    421 attcagcgtc aacgtaaaag tagctactgc aacacattg ggcgtgtaac gtaagtcagg
    481 gtccttagtt aaacgaccaa cgaggataac acgattcatt aa

```

//

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

5224259..5224260 | 1



Search **Nucleotide** for **Limits** **Preview/Index** **History** **Clipboard** **Details**
 Display **GenBank(Full)** Show **5** Send to
 Projection on the feature (#6) Show whole Sequence Features: + Refresh

☐ 1: NZ_AAOY01000054. Reports *Bacillus weihenst...*[gi:89207994]

Links

Comment Features Sequence

LOCUS NZ_AAOY01000054 522 bp DNA linear BCT 06-MAR-2006
 DEFINITION *Bacillus weihenstephanensis* KBAB4 ctg231, whole genome shotgun
 sequence.
 ACCESSION NZ_AAOY01000054 REGION: complement(5415..5936)
 VERSION NZ_AAOY01000054.1 GI:89207994
 KEYWORDS WGS.
 SOURCE *Bacillus weihenstephanensis* KBAB4
 ORGANISM *Bacillus weihenstephanensis* KBAB4
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus
 cereus group.
 REFERENCE 1 (bases 1 to 522)
 AUTHORS Lapidus,A., Goltsman,E., Copeland,A., Lucas,S., Barry,K.,
 Dettler,J.C., Glavina del Rio,T., Hammon,N., Israni,S., Dalin,E.,
 Tice,H., Bruce,D., Pitluck,S., Richardson,P., Auger,S.,
 Galleron,N., Sanchis,V., Gohar,M., Broussole,V., Brillard,J.,
 Guinebretiere,M.-H., Ehrlich,S.D., Lereclus,D., Aymerich,S.,
 Nguyen-the,C. and Sorokin,A.
 CONSRTH US DOE Joint Genome Institute (JGI-PGF)
 TITLE Sequencing of the draft genome and assembly of *Bacillus*
weihenstephanensis KBAB4
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 522)
 AUTHORS Larimer,F. and Land,M.
 CONSRTH US DOE Joint Genome Institute (JGI-ORNL)
 TITLE Annotation of the draft genome assembly of *Bacillus*
weihenstephanensis KBAB4
 JOURNAL Unpublished
 REFERENCE 3 (bases 1 to 522)
 AUTHORS Lapidus,A., Goltsman,E., Copeland,A., Lucas,S., Barry,K.,
 Dettler,J.C., Glavina del Rio,T., Hammon,N., Israni,S., Dalin,E.,
 Tice,H., Bruce,D., Pitluck,S., Richardson,P., Auger,S.,
 Galleron,N., Sanchis,V., Gohar,M., Broussole,V., Brillard,J.,
 Guinebretiere,M.-H., Ehrlich,S.D., Lereclus,D., Aymerich,S.,
 Nguyen-the,C. and Sorokin,A.
 CONSRTH US DOE Joint Genome Institute (JGI-PGF)
 TITLE Direct Submission
 JOURNAL Submitted 02-MAR-2006 US DOE Joint Genome Institute, 2800
 Mitchell Drive B100, Walnut Creek, CA 94598-1698, USA
 COMMENT URL -- <http://www.jgi.doe.gov>
 Contact: Paul Richardson (microbes@cuba.jgi-psf.org)
 Draft sequencing done at US DOE Joint Genome Institute
 Source DNA and bacteria available from Alexei Sorokin
 (alexsei.sorokine@jouy.inra.fr)

The JGI and collaborators endorse the principles for the distribution and use of large scale sequencing data adopted by the larger genome sequencing community and urge users of this data to follow them. It is our intention to publish the work of this project in a timely fashion and we welcome collaborative interaction on the project and analysis.

(<http://www.genome.gov/page.do?pageID=10506376>)

Notes:

Bacillus weihenstephanensis KBAB4 was originally isolated from forest soil near Versailles, France, and was originally identified as *Bacillus cereus* (Vilas-Boas et al, Appl Env Microbiol, 2002, 68, 1414). More detailed phylogenetic analysis, using MLST, of the Versailles Collection of *B. cereus* and *B. thuringiensis* strains revealed that the strain grows at low temperature (60C) and clusters with many other strains able to grow at low temperatures, including the independently isolated and characterized strains WSB010204 and WSB010206 (Sorokin et al, Appl Env Microbiol, 2006, 72, 1569). The latter two strains are the type strains of a newly recognized species in the *B. cereus* group able to grow in cold and having the species name *Bacillus weihenstephanensis* (Lechner et al, Int. J. Syst. Bacteriol, 1998, 48, 1373). Since, by MLST, KBAB4 is very closely related to WSB010204 and represents many other psychrotrophic strains, it was assigned a species name *Bacillus weihenstephanensis* and the strain KBAB4 should also be considered as a type representative of this species.

```
FEATURES
    source            Location/Qualifiers
                        1..522
                        /organism="Bacillus weihenstephanensis KBAB4"
                        /mol_type="genomic DNA"
                        /strain="KBAB4"
                        /db_xref="taxon:315730"
    gene              1..522
                        /locus_tag="BcerKBAB4DRAFT_2050"
    CDS                1..522
                        /locus_tag="BcerKBAB4DRAFT_2050"
                        /codon_start=1
                        /transl_table=11
                        /product="Single-strand binding protein"
                        /protein_id="WP_01186525.1"
                        /db_xref="GI:89208000"
                        /db_xref="InterPro:IPR000424"
                        /db_xref="InterPro:IPR004365"
                        /db_xref="InterPro:IPR010913"
                        /db_xref="InterPro:IPR011344"
                        /translation="MMNRVILVGLTKDPLDRLYPNGVAVATFTLAVNRAFAANQQGER
EADFINCVINRKAENVANYLKKGSLAGVDGRLQTRNYDQDGKRVYVTEVLAEVSQF
LEPRNGGGEQRGSFENQPSGAGFGNQSSNFFGQSSNSGNQNGNSGFTKNDPFSNV
GQPIDISDDLLPF"
```

ORIGIN

```
1 ttgataagc gtgttatct cgttggtcgt ttaactaagg accctgaact acgtttacaag
61 cccaatgggt ttgcagtagc tactttttac ttgctgtgta atcgcgcatc tgcgaatcaa
121 caaggtgagc gtgaagctga ctttattaat tgtgtaatat ggcgtaaaaca agcagaaaac
181 gggcgaact atttgaaaaa aggtagcttta gcagggcgtag acggagctct tbaacttcgt
241 aattacgagc gacaagatgg taacagtgtg tatgtaacag aagttotttc ggagagcgtg
301 caatttttag agcccggtaa tggcggtggg gacgaacgtg gtccattcaa tgcgaacca
361 tcaggagcgtg gtttcggtga ccaagctctt aaccoatttg gtaactotag taattcaggt
421 aaccaagcta atcaaggtaa ctctggattt acgaagaatg acgatccatt ttggaaggtt
481 ggtcaaccga ttgacatttc ggaagacgat ttacattttt aa
```

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

July 31/2006 12:12:14





[Pharm](#)
[Nucleotide](#)
[Protein](#)
[Genome](#)
[Structure](#)
[PMC](#)
[Taxonomy](#)
[Jvarkit](#)
[Books](#)

[Search Nucleotide](#)
[for](#)
[Limits](#)
[Preview/Index](#)
[History](#)
[Clipboard](#)
[Details](#)

[Go](#)
[Clear](#)

Display [GenBank\(Full\)](#) [Show 5](#) [Send to](#)

Projection on the feature (#184)

[Show whole Sequence](#)

Features: + [Refresh](#)

☐ I: Z99124. Reports *Bacillus subtilis*...[gi:32468840]

[Links](#)

[Comment](#) [Features](#) [Sequence](#)

LOCUS PSUB0021 519 bp DNA linear BCT 18-APR-2005
DEFINITION *Bacillus subtilis* complete genome (section 21 of 21): from 4010730 to 4214630.
ACCESSION Z99124 REGION: complement(187181..187699)
VERSION Z99124.2 GI:32468840
KEYWORDS .
SOURCE *Bacillus subtilis* subsp. *subtilis* str. 168
ORGANISM *Bacillus subtilis* subsp. *subtilis* str. 168
REFERENCE Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
AUTHORS 1 (bases 1 to 519)
 Kunst, F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertero, M.G., Bessieres, P., Bolotin, A., Borchert, S., Borries, R., Boursier, L., Brans, A., Braun, M., Brignell, S.C., Bron, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, F., Devine, K.M., Dusterhoft, A., Ehrlich, S.D., Emmerson, P.T., Entian, K.D., Errington, J., Fabret, C., Fazzari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galleron, N., Ghim, S.Y., Glaser, P., Goffeau, A., Gollightly, E.J., Grandi, G., Guiseppe, G., Guy, B.J., Haga, K., Halech, J., Harwood, C.R., Henaut, A., Hilbert, H., Holsappel, S., Hosono, S., Hulio, M.F., Itaya, M., Jones, L., Joris, B., Karamata, D., Kasahara, Y., Klaerr-Blanchard, M., Klein, C., Kobayashi, Y., Koetter, P., Koringsstein, G., Krogh, S., Kumano, M., Kurita, K., Lapidus, A., Lardinois, S., Lauber, J., Lazarevic, V., Lee, S.M., Levine, A., Liu, R., Masuda, S., Mauel, C., Medigue, C., Medina, N., Mellado, R.P., Mizuno, M., Moestl, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, A., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Portetelle, D., Porwollik, S., Prescott, A.M., Presecan, E., Pujic, P., Purnelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M., Rivolta, C., Rocha, E., Roche, B., Rose, M., Sadale, Y., Sato, T., Scanlan, E., Schleich, S., Schroeter, K., Scoffone, P., Sekiguchi, J., Sekowska, A., Seror, S.J., Serror, P., Shin, B.S., Soldo, B., Sorokin, A., Taccioni, E., Takagi, T., Takahashi, H., Takemaru, K., Takeuchi, M., Takakoshi, A., Tanaka, T., Terpstra, P., Tognoni, A., Tosato, V., Uchiyama, S., Vandenbol, M., Vannier, F., Vassarotti, A., Viari, A., Wambutt, R., Wedler, E., Wedler, H., Weltzenegger, T., Winters, P., Wipat, A., Yamamoto, H., Yamane, K., Yasumoto, K., Yata, K., Yoshida, K., Yoshikawa, H.F., Zumstein, E., Yoshikawa, R. and Danchin, A.
TITLE The complete genome sequence of the gram-positive bacterium *Bacillus subtilis*
JOURNAL Nature 390 (6657), 249-256 (1997)

```

FORMED 9241317
REFERENCE 2 (bases 1 to 519)
AUTHORS Kunst, F., Ogasawara, N., Yoshikawa, R. and Danchin, A.
TITLE Direct Submission
JOURNAL Submitted (27-JUN-2003) I. Moszer, A. Danchin, Institut Pasteur,
Genetique des Genomes Bacteriens, 28 rue du Docteur Roux, 75724
Paris Cedex 15, FRANCE. E-mail: moszer@pasteur.fr,
adanchin@pasteur.fr Phone: +33 (0)1 45 69 84 41, Fax: +33 (0)1 45
68 89 48
COMMENT On Jul 7, 2003 this sequence version replaced gi:2430442.
This entry contains data from release R16.1 of the Subtilist
database. Further data on gene annotation and detailed information
about changes from previous releases can be found at
http://genolist.pasteur.fr/Subtilist/.
FEATURES
    Location/Qualifiers
        source
            1..519
            /organism="Bacillus subtilis subsp. subtilis str. 168"
            /mol_type="genomic DNA"
            /strain="168"
            /db_xref="taxon:224339"
        gene
            1..519
            /gene="ssb"
            /locus_tag="BSU40900"
        CDS
            1..519
            /gene="ssb"
            /locus_tag="BSU40900"
            /codon_start=1
            /transl_table=11
            /product="single-strand DNA-binding protein"
            /protein_id="CAB16127.1"
            /db_xref="GI:2636637"
            /db_xref="GOA:P37455"
            /db_xref="InterPro:IPR000424"
            /db_xref="InterPro:IPR008994"
            /db_xref="InterPro:IPR010913"
            /db_xref="Subtilist:BG10048"
            /db_xref="UniProtKB/Swiss-Prot:P37455"
            /translation="MLNRVVLVGLTKDFELRYTFNGAAVATFTLAVNRFTNQSGER
            EADPINCVTNRQAEENVANFLKKGLAGVDGRLQTRNYENQQGQRVFEVTEVQAESVQF
            LEPKNGGGSGSGGYNEGNSGGGQYFGGQNDNPFPGGNQNNQFRNQNSFNDDPFANDG
            KPIIDISDDDLFF"
ORIGIN
1 atgcttaaac gagttgtatt agtcggaaga ctgacaaaag acccagagct tcgttatagc
61 ccaaaacgggt cggctgttgc taagtattact cttgctgtga atcgtaacatt tacgaaccag
121 tcocggagaac gtgaggccga ttctattaat tgtgtcaact ggagaagaca acccgaaaac
181 gttgcacaact tcttgaaaaa aggaagccctt gcaggcgtag atggcggttt acaacaaga
241 aactatgaaa accagcaagg acagcgtgtc tctgtgacag aggtccaacg tgaagtgtt
301 caatttcttg agccgaaaaa cggcgccggt tctggttcag gtggatacaa cgaaggaaac
361 agcggcgagg gccactactt tggcggaggg caaatgata atccatttgg gggaaatcaa
421 aacaaccaga gacgcaatca ggggaacagc tttaatgatg acccatttgc caacgacggc
481 aaaccgattg acatctcgga tgatgatctt ccattcttaa

```

//

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

Jul 24 2003 14:14






[Portals](#) [Nucleotide](#) [Protein](#) [Genome](#) [Structure](#) [PMC](#) [Taxonomy](#) [GSM](#) [Books](#)

Search **Nucleotide** for **Go** **Clear**

[Limits](#) [Preview/Index](#) [History](#) [Clipboard](#) [Details](#)

Display **GenBank(Full)** Show **5** [Send to](#)

Range: from **4206965** to **4207477** [Show whole sequence](#) [Reverse complemented str.](#)

1: CP000002. Reports Bacillus lichenif...[gi:56160984]

[Links](#)

Comment Features Sequence

LOCUS CP000002 513 bp DNA linear RCT 03-DEC-2004
DEFINITION Bacillus licheniformis ATCC 14580, complete genome.
ACCESSION CP000002 REGION: 4206965..4207477
VERSION CP000002.2 GI:56160984
KEYWORDS .
SOURCE Bacillus licheniformis ATCC 14580 (DSM 13)
ORGANISM Bacillus licheniformis ATCC 14580
 Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
REFERENCE 1 (bases 1 to 513)
AUTHORS Rey,M.W., Ramaiya,P., Nelson,B.A., Brody-Karpin,S.D.,
 Zaretsky,E.J., Tang,M., de Leon,A.L., Xiang,H., Gusti,V.,
 Clausen,I.G., Olsen,P.B., Rasmussen,M.D., Andersen,J.T.,
 Jorgensen,P.L., Larsen,T.S., Sorokin,A., Bolotin,A., Lapidus,A.,
 Galleron,N., Ehrlich,S.D. and Berka,R.M.
TITLE Complete genome sequence of the industrial bacterium Bacillus
 licheniformis and comparisons with closely related Bacillus species
JOURNAL Genome Biol. 5 (10), R77 (2004)
 PUBMED 15461803
REFERENCE 2 (bases 1 to 513)
AUTHORS Berka,R.M., Rey,M.W. and Ramaiya,P.
TITLE Direct Submission
JOURNAL Submitted (14-JUL-2004) Novozymes Biotech Inc, 1445 Drew Ave,
 Davis, CA 95616, USA
REFERENCE 3 (bases 1 to 513)
AUTHORS Berka,R.M., Rey,M.W. and Ramaiya,P.
TITLE Direct Submission
JOURNAL Submitted (29-SEP-2004) Novozymes Biotech Inc, 1445 Drew Ave,
 Davis, CA 95616, USA
REMARK Sequence update by submitter
COMMENT On Dec 1, 2004 this sequence version replaced gi:52001702.
FEATURES Location/Qualifiers
 source
 1..513
 /organism="Bacillus licheniformis ATCC 14580"
 /mol_type="genomic DNA"
 /strain="ATCC 14580; DSM 13"
 /db_xref="ATCC:14580"
 /db_xref="taxon:279013"
 /focus
 gene
 complement(1..513)
 /gene="ssb"
 /locus_tag="BL00099"
 CDS
 complement(1..513)
 /gene="ssb"


```

/locus_tag="BL00099"
/note="InterProMatches:IPR000424; Molecular Function:
single-stranded DNA binding (GO:0003697)"
/codon_start=1
/translation_table=1
/product="single-strand DNA-binding protein"
/protein_id="AAC1798.1"
/db_xref="GI:52005846"
/translation="MLNRVVLVGRLLTKQPELRYTFSGAAVATFTLAVNRFTNQQGER
EALFINCVVWRQAENVANFLKKGLAGVDGRLQTRSYENQQQRRVYVTEVQAESVQF
LEPKGGSGSGGYSGGQGGQRFGGGQNEPAPFGSGQNNQNRNQGNSFNDDPFANDCKP
IDISDDDLFF"

```

ORIGIN

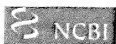
```

1  ttaaaatggc aagtcgtcat cagagatgta aatcggcttt ccatcatttg cgaatggatc
61  gtcatcgaag ctgttgcctt gattggcatt ctgattgttt tgactgcgcg cgaatggagc
121  cggttcattt tatcgcgcgc aaaaagtgtg gctcccttgg cctccgctgt aacgcgcgga
181  accagaaacg ccgcctttag gctccagaaa ttgaacactt tcagcttgaa ctcccgtagc
241  gtatacacgc tgtccctgct gattttcata gctgcgcgtt tgcaaacctc catctacacc
301  cgcagagactt ccttttttaa ggaattttgc aacgttttgc gottgtcttc tccagacacc
361  acagttgatg aaatcagctt cagcttcacc ctgctgatto gtaaacgtac gattgacaga
421  aagcgtaaag dtggcaacag ctgcaccgct aggaagtata cgaagctctg ggtcctttgt
481  cagctcgcgc actaaaacaa ctgcgttaag cat

```

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

Aug 24, 2006 17:22:14



My NCBI
[Sign In]
[Register]

Search Nucleotide

for

Go

Clear

Limits

Preview/Index

History

Clipboard

Details

Display GenBank(Full)

Show 5

Send to

Range: from 4186205

to 4186711

Show whole sequence

☐ Reverse complemented str1: BA000004. Reports *Bacillus halodurans*...[gi:47118318]

Links

Comment Features Sequence

LOCUS BA000004 507 bp DNA linear BCT 01-DEC-2004
 DEFINITION *Bacillus halodurans* C-125 DNA, complete genome.
 ACCESSION BA000004 REGION: 4186205..4186711
 VERSION BA000004.3 GI:47118318
 KEYWORDS
 SOURCE *Bacillus halodurans* C-125
 ORGANISM *Bacillus halodurans* C-125
 Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 REFERENCE 1
 AUTHORS Takami, H.
 TITLE Genome analysis of facultatively alkaliphilic *Bacillus halodurans* C-125
 JOURNAL (in) Horikoshi, K. and Tsujii, K. (Eds.);
 EXTREMOPHILES IN DEEP-SEA ENVIRONMENTS: 249-284;
 Springer-Verlag (1999)
 REFERENCE 2
 AUTHORS Takami, H. and Horikoshi, K.
 TITLE Reidentification of facultatively alkaliphilic *Bacillus* sp. C-125
 to *Bacillus halodurans*
 JOURNAL Biosci. Biotechnol. Biochem. 63, 943-945 (1999)
 REFERENCE 3
 AUTHORS Takami, H., Nakasone, K., Hiram, C., Takaki, Y., Masui, N., Fuji, F.,
 Nakamura, Y. and Inoue, A.
 TITLE An improved physical and genetic map of the genome of alkaliphilic
Bacillus sp. C-125
 JOURNAL Extremophiles 3 (1), 21-28 (1999)
 PUBMED 10086643
 REFERENCE 4
 AUTHORS Takami, H., Nakasone, K., Ogasawara, N., Hiram, C., Nakamura, Y.,
 Masui, N., Fuji, F., Takaki, Y., Inoue, A. and Horikoshi, K.
 TITLE Sequencing of three lambda clones from the genome of alkaliphilic
Bacillus sp. strain C-125
 JOURNAL Extremophiles 3 (1), 29-34 (1999)
 PUBMED 10086642
 REFERENCE 5
 AUTHORS Takami, H., Takaki, Y., Nakasone, K., Hiram, C., Inoue, A. and
 Horikoshi, K.
 TITLE Sequence analysis of a 32-kb region including the major ribosomal
 protein gene clusters from alkaliphilic *Bacillus* sp. strain C-125
 JOURNAL Biosci. Biotechnol. Biochem. 63 (2), 452-455 (1999)
 PUBMED 10192928
 REFERENCE 6
 AUTHORS Takami, H., Masui, N., Nakasone, K. and Horikoshi, K.

TITLE Replication origin region of the chromosome of alkaliphilic
 Bacillus halodurans C-125
 JOURNAL Biosci. Biotechnol. Biochem. 63 (6), 1134-1137 (1999)
 PUBMED 10484179
 REFERENCE 7
 AUTHORS Takami,H., Takaki,Y., Nakasone,K., Sakiyama,T., Maeno,G.,
 Sasaki,R., Hirama,C., Fuji,F. and Masui,N.
 TITLE Genetic analysis of the chromosome of alkaliphilic Bacillus
 halodurans C-125
 JOURNAL Extremophiles 3 (3), 227-233 (1999)
 PUBMED 10484179
 REFERENCE 8
 AUTHORS Takami,H. and Horikoshi,K.
 TITLE Analysis of the genome of an alkaliphilic Bacillus strain from an
 industrial point of view
 JOURNAL Extremophiles 4 (2), 99-108 (2000)
 PUBMED 10805564
 REFERENCE 9
 AUTHORS Nakasone,K., Masui,N., Takaki,Y., Sasaki,R., Maeno,G., Sakiyama,T.,
 Hirama,C., Fuji,F. and Takami,H.
 TITLE Characterization and comparative study of the rxn operons of
 alkaliphilic Bacillus halodurans C-125
 JOURNAL Extremophiles 4 (4), 209-214 (2000)
 PUBMED 10372199
 REFERENCE 10
 AUTHORS Takami,H., Nakasone,K., Takaki,Y., Maeno,G., Sasaki,R., Masui,N.,
 Fuji,F., Hirama,C., Nakamura,Y., Ogasawara,N., Kuhara,S. and
 Horikoshi,K.
 TITLE Complete genome sequence of the alkaliphilic bacterium Bacillus
 halodurans and genomic sequence comparison with Bacillus subtilis
 JOURNAL Nucleic Acids Res. 28 (21), 4317-4331 (2000)
 PUBMED 11059152
 REFERENCE 11 (bases 1 to 507)
 AUTHORS Takami,H. and Takaki,Y.
 TITLE Direct Submission
 JOURNAL Submitted (22-MAR-2000) Hideto Takami, Japan Marine Science and
 Technology Center, Deep-sea Microorganisms Research Group; 2-15
 Natsushima, Yokosuka, Kanagawa 237-0061, Japan
 (E-mail:takamih@jamstec.go.jp,
 URL:http://www.jamstec.go.jp/jamstec-e/bio/DEEPSTAR/FResearch.html,
 Tel:81-468-67-3895, Fax:81-468-66-6364)
 COMMENT On or before Dec 8, 2004 this sequence version replaced
 gi:10172612, gi:10172890, gi:10173176, gi:10173440, gi:10173701,
 gi:10174030, gi:10174345, gi:10174613, gi:10641879, gi:10175102,
 gi:10175500, gi:10175792, gi:10176109, gi:10176401.
 FEATURES
 source
 1..507
 /organism="Bacillus halodurans C-125"
 /mol_type="genomic DNA"
 /strain="C-125"
 /db_xref="taxon:272558"
 /note="alkaliphile"
 gene
 complement(1..507)
 /gene="ssb"
 CDS
 complement(1..507)
 /gene="ssb"
 /note="BH4049"
 /codon_start=1
 /transl_table=11
 /product="single-strand DNA-binding protein (phage-related)

```

protein)"
/protein_id="9685729.1"
/db_xref="GI:10176674"
/translation="MLNRVVLVGPLTRDPELRYTPNGYAVANPTLAVNRPFNSQGER
EAGFVNCVYWRKQAEVANYLKKGLACVDSRIQTRSYDMMEGRRTVTE/MAESVQF
LEPRGSGSQGGSHVDNFGGSGPNNPMSGNDPQSGSGSGPQSGGSEDFPANDGRID
ISDDDLRF"
ORIGIN
1  ttagaatggc  aatcatcat  cggaaatata  gattgggttg  ccatcatttg  caaacgggtc
61  ttctgagaaa  caccgggatt  gacgtccgga  gccaccagat  tgttgccaga  aatcattacc
121  gcccatgggg  ttgttagggg  agccggccac  aaagtctgta  acgtttgata  ccccttggtt
181  ttgtgagcgg  cgcggttcaa  ggaattgaac  gctttctgac  atgacctctg  tcacaaagac
241  tctggggcct  tcattgttgt  cataactgag  cgtttgaata  cgaacctcaa  caaacagtag
301  acttcccttt  tcaaatagt  tcgccacgtt  ctccggttgc  tcgcgcacaa  cgaacagttt
361  aatgaaatct  gcttcgcgct  ctcttctgtg  gttcgagaac  gggcggttta  cagcaaggtt
421  aaagtgttgc  acagcaacac  cgtttggcgt  gtacgcgaac  tcggatcac  gtttcaacgg
481  accgaactagg  acgacacgat  ttaacat
//

```

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

Jul 24 2006 17:22:14






Search Nucleotide for Go Clear

Limits Preview/Index History Clipboard Details

Display GenBank(Full) Show 5 Send to

Range: from 4288801 to 4289286 Show whole sequence ☐ Reverse complemented str.

1: AP006627. Reports *Bacillus clausii* ...[gi:56908016]

Links

Features Sequence

LOCUS AP006627 486 bp DNA linear BCT 28-JUL-2006
 DEFINITION *Bacillus clausii* KSM-K16 DNA, complete genome.
 ACCESSION AP006627 REGION: 4288801..4289286
 VERSION AP006627.1 GI:56908016
 KEYWORDS
 SOURCE *Bacillus clausii* KSM-K16
 ORGANISM *Bacillus clausii* KSM-K16
 Bacteria; Firmicutes; Bacillales; Bacillaceae; *Bacillus*.
 REFERENCE 1
 AUTHORS Hakamada, Y., Kobayashi, T., Hitomi, J., Kawai, S. and Ito, S.
 TITLE Molecular cloning and nucleotide sequence of the gene for an alkaline protease from the alkaliphilic *Bacillus* sp. KSM-K16
 JOURNAL J. Ferment. Bioeng. 78, 105-108 (1994)
 REFERENCE 2
 AUTHORS Kobayashi, T., Hakamada, Y., Adachi, S., Hitomi, J., Yoshimatsu, T., Koike, K., Kawai, S. and Ito, S.
 TITLE Purification and properties of an alkaline protease from alkaliphilic *Bacillus* sp. KSM-K16
 JOURNAL Appl. Microbiol. Biotechnol. 43 (3), 473-481 (1995)
 PUBMED 7652397
 REFERENCE 3
 AUTHORS Shirai, T., Suzuki, A., Yamane, T., Ashida, T., Kobayashi, T., Hitomi, J. and Ito, S.
 TITLE High-resolution crystal structure of M-protease: phylogeny aided analysis of the high-alkaline adaptation mechanism
 JOURNAL Protein Eng. 10 (6), 627-634 (1997)
 PUBMED 9278275
 REFERENCE 4
 AUTHORS Sakaki, Y., Kageyama, Y., Shimamura, S., Suzuki, H., Nishi, S., Hatada, Y., Kawai, S., Ito, S. and Horikoshi, K.
 TITLE The complete genome sequence of the alkaliphilic *Bacillus clausii* KSM-K16
 JOURNAL Unpublished
 REFERENCE 5 (bases 1 to 486)
 AUTHORS Sakaki, Y., Kageyama, Y., Shimamura, S., Suzuki, H., Nishi, S., Hatada, Y., Kawai, S., Ito, S. and Horikoshi, K.
 TITLE Direct Submission
 JOURNAL Submitted (19-OCT-2003) Yasushi Kageyama, Kao Corporation, Biological Science Laboratories; 2606 Akabane, Ichikai-machi, Hago-gun, Tochigi 321-3497, Japan
 :E-mail:kageyama.yasushi@kao.co.jp, URL:http://www.kao.co.jp/e/, Tel:81-285-68-7516, Fax:81-285-68-7547)
 FEATURES Location/Qualifiers

```

source      1..486
             /organism="Bacillus clausii KSM-K16"
             /mol_type="genomic DNA"
             /strain="KSM-K16"
             /db_xref="taxon:56642"
             /note="alkaliophile"
gene        complement(1..486)
             /gene="ssb"
             /locus_tag="ABC4106"
CDS         complement(1..486)
             /gene="ssb"
             /locus_tag="ABC4106"
             /codon_start=1
             /transl_table=11
             /product="single-strand DNA-binding protein SSB"
             /protein_id="BAD68837.1"
             /db_xref="GI:56912109"
             /translation="MLNRVVLVGRLLTRDPFLRFTFNGVAVANFTLAVNRFPSNQOGER
EADFINCVWRKPAENVANFLKKGSLAGVDGRVQTRSYDNNEGRVVFVTEIVAESVQF
LEPRNSQNQSGGNNPQFDQYGAGNQGSGNQTGGRSNGYDNDPFSNDGSDIDSDDDLP
E"
ORIGIN
1  ttaaaatgga  agatcatcgt  cggaaatata  aatcgaaaccg  toatttcgaga  acgggttcgt
61  atcatatcca  ttagaacggc  tgccaccagt  ttggttgcca  gaacatttgt  tgccagcgcc
121  gtactgatca  aaaccaaggat  tattccacga  ggatttggtt  tgactgttgc  gaggttcgag
181  aaattggacg  ctttcagcaa  cgatttcctg  tacaataaacg  cgcctgcott  cattattgtc
241  atagcttcgc  gtttgacac  ggccttgac  tccctgcaag  ctcctctttt  taaggaaatt
301  ggcgacgttc  tcagccggtt  tgcccgacac  aacacagtta  atgaagtcag  cttctcgttc
361  tccctgtgtg  ttgaaaacg  gacggttgac  tgcagcgta  aaattggcta  cagctacacc
421  gtttggcgtg  aatgcgaatt  cagggttcacg  cgtaaagcgt  ccgacaagaa  caacacgggt
481  taacaa
//

```

Disclaimer | Write to the Help Desk
NCBI | NLM | NIH

Jun 24 2009 11:11:13

EXHIBIT 2

```

#####
# Program:   needie
# Rundate:   Mon Jul 31 06:58:16 2006
# Align_format: srspair
# Report_file: /ebi/extserv/cld-work/needie-20060731-06581567407497.output
#####

```

```
#
# Aligned_sequences: 2
# 1: SEQ175
# 2: G_kausotophilus
# Matrix: EBL0SGM2
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 553
# Identity: 252/553 (45.6%)
# Similarity: 252/553 (45.6%)
# Score: 119/553 (21.5%)
#
```

SEQ175	1	atgattaacccgctc-----attttggtggcgagg-----ttaa	34
G_kausetphilu	1	ttaaaacggcaaatctcatcagaaatatcgatcggtctgcgcgtcatttg	50
SEQ175	35	cgaga-gatc-----cggagttcgcttaaac-----tcaacggga-----g	70
G_kausetphilu	51	cgaaaggatcgctcatcgatcgcgcaaacacctttttcgttcggatatgg	100
SEQ175	71	tgg--ctg-----ttgcacgttttac-----ctcgcggtcaaccgtc-	106
G_kausetphilu	101	tggttctgatcttgc-cgaatgggaatggatcccatat-agccgcct	148
SEQ175	107	-cgtttacaatcagcagggcgagcggg--aaacggattttatcaatgt	153
G_kausetphilu	149	gtgcttgccctc-gotgctgcctgcttctcttcggc--tcaagaaattg	195
SEQ175	154	gtcgtttggcgcgcga-----ggcg-gaaaacgtcgccaattttgaa	197
G_kausetphilu	196	gaacgtatcagcagcaacttcgctcagctacacg-cgcgcacctcttga	244
SEQ175	198	aaaggggagcttggtcg--tgtcgatggcgcgtcgaacccgcg--agc	243
G_kausetphilu	245	tttccatagt--gcgggttcgaatcgccatcgac--accagccaagc	290
SEQ175	244	tatgaaaatacaagaggtgcggt-gtgtacgtgcagcgaagtgtgtgctg	292
G_kausetphilu	291	tcccttttttcaaaagttgcgcagacttttc-cgac-----tgcgcgcg	334
SEQ175	293	atagcgtccaatattcttgag--ccgaagaaggacgcagcagcggagg	340
G_kausetphilu	335	caaacgcacatgaaataaatacgttt--ccgcctgcgcctgc-tgatt	381
SEQ175	341	cgacagcaggcgctg-actatggggatccattcccatcgggcgaagatca	389
G_kausetphilu	382	tgtcaacggcagcgttgaccgcgag--cgtaaacgt--ggcaaa--ca	421

SEQ175	330	gaacccccaatattccgaacagcaaaagggttttcggccatcgatgagcgc	439
		
G_kausotphilu	422	g--ccac-----tcgcgttg-----gaggtt-aagcgcaac--tcgcgat	455
SEQ175	440	ctttccccaattgacggcagccgcatcgattttctgatgagtgatttcggc	489
		
G_kausotphilu	456	ctctcgttaaa-----cctgcgcaccaaatgac-gcggttaat-----ca	494
SEQ175	490	ttt	492
G_kausotphilu	495	t	495

```

##
# Program: needle
# RunDate: Mon Jul 31 07:12:56 2006
# Align_format: srspair
# Report_file: /ebi/outserv/old-work/needle-20060731-0712551097974.output
##

```

```

##
#

```

```

# Aligned_sequences: 2
# 1: SEQ175
# 2: B_cereus
# Matrix: EBL0SUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 583
# Identity: 246/553 (44.5%)
# Similarity: 246/553 (44.5%)
# Gaps: 101/553 (18.3%)
# Score: 1047.0
#

```

```

##

```

```

SEQ175      1      atgattaaccg-cgtcattttggtcggcagggttaacgagagatcc      44
              |.|.|.|.| | | | | | | | | | | | | | | | | | | | |
B_cereus    1      ttagaacggttaaatcgtcgtcggaatgtcgatcggttgac-ctacatt      49

SEQ175      45     ggaggttg---cgttacactcc---aaagcgagtggtc---gttgccacg      84
              |.|.| | | | | | | | | | | | | | | | | | | | | |
B_cereus    50     gaaatggatcgtcattcttcgttaaatccagagttaccttggtttacctga      99

SEQ175      85     tttaacgtcgcgggtcaaccg-----tcc---gtttacaacacgacagg      124
              .| | | | | | | | | | | | | | | | | | | | | | | |
B_cereus    100    attactagattgaccaaattgggttagacgttggtttaccgaaac--cagc      147

SEQ175      125    gcgagcgggaaacggattttttatcaattgtgtcgtttggcgccca----      170
              .|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|.|
B_cereus    148    tcttgatggtgtgtcgtattaaatgaaccagttgctccccacgcattac      197

SEQ175      171    --ggcggaataacgtcgccaatttttgaanaaggggagcgttggtcgt----      214
              | | | | | | | | | | | | | | | | | | | | | | | |
B_cereus    198    gcggtctaaaaattgcacgttttcgcaa----gaactt--ctgttac      240

SEQ175      215    gtgt---cgatggcgactgcgcaaacccgcagctatgaaatacaagaaggt      261
              | | | | | | | | | | | | | | | | | | | | | | | |
B_cereus    241    gtatacagtttaccattctgttcctcgttaattacaggtttgaagacgcc      290

SEQ175      262    cggcgtgtgtacgtacggaagtggtggtgctgatacgtccaatttcttga      311
              |.| | | | | | | | | | | | | | | | | | | | | | |
B_cereus    291    catc----tac--gcctgctaagctaaccttttt---tcaataaatttgc      330

SEQ175      312    gccgaaaggaaacgagcgcagcgagcgaggcgagaca-----gcagcggtc      355
              .| | | | | | | | | | | | | | | | | | | | | | | |
B_cereus    331    tacgtttttcgtgttttaacgcacattac--acaattaataagtcagct      379

SEQ175      356    actarggggatccattccatttcgggcaagatc-agaacccacaaatacc      404
              .| | | | | | | | | | | | | | | | | | | | | | | |
B_cereus    380    tcac--gctcaccttgctgatt--ggcaaatgcggcatcacag-----c      420

```

SEQ175	448	gaacgaaaaaggggtttggcgcgatcgatgacgacatcctttgcgaatgacg	454
B_cereus	421		
	421	taacgtaaaag----tagctactcgg---gac-accat gggggtgtaacg	462
SEQ175	455	---gcacgcgcgatcgatattt-----ctgagtgatctatttgcggctt	492
B_cereus	463		
	463	taagttag- -ggctccttagt taaacgaccaacgaggataaacagcattcat	510
SEQ175	493	492	
B_cereus	511	caa	513

#####

Program: needle
RunDate: Mon Jul 31 07:14:27 2006
Align_format: srapair
Report_file: /ebi/extern/old-work/needle-20060731-0714262184817C.output
#####

#####

Aligned_sequences: 2
1: SEQ175
2: B_anthraxis
Matrix: EBI6SUM62
Gap_penalty: 10.0
Extend_penalty: 0.5

Length: 577
Identity: 237/577 (41.1%)
Similarity: 237/577 (41.1%)
Gaps: 131/577 (22.7%)
Score: 1040.5
#

#####

SEQ175	1	atgattaaacgc-cgtcattttggtcgcaggttaacgagagatcc	44
B_anthraxis	1	ttagaacggttaaatcgtcgtcggaaatgtcgatcggttgac-ctacattt	49
SEQ175	45	ggagttg---cgttaacactcc---aagcggagtggt---gttgccacg	84
B_anthraxis	50	gaaaatggatcgtcattcttcgtaaatccagagtttcttgggtacattt	99
SEQ175	85	tttaacgc-----tcgcggtcaacc-----gtcc---gtttacaa	115
B_anthraxis	100	gttgcccaattactagattgaccaaatgggttagagcttgggttaacga	149
SEQ175	116	atcagcaggggagcggggaacggattttatcaatgtcgtttgggcg	165
B_anthraxis	150	aac--cagctcctgatgggtgctgattaaatgaaccacgttgctccccc	197
SEQ175	166	cgcca-----ggcggaaacgtcgccaacttttgaiaaaggaggctt	209
B_anthraxis	198	cgccattacgcggctctaaaaattgtacgcttccggca-----gaactt	242
SEQ175	210	ggctggtgtcgatggcgcgactgcaaacccgcagctatgaaatcaagaag	259
B_anthraxis	243	--ctgttacataacacgcttaccattcttgcctcgttaattacagattt	290
SEQ175	260	gtcggcgtgtgtacgtgacgggaagtgggtgct-----gatagcg	298
B_anthraxis	291	gaagacgtccatcatcgcgctgctgaagctacatttttttaaatatttgc-	339
SEQ175	299	tccaatctc-----ttgagccgaaaggaaacgagcga-----gcagcga	336
B_anthraxis	340	tacgtttctcgtctgtttacgccatattacacattataaagctcagctt	389
SEQ175	337	ggggcgacagagggcggtactactggggatccattccca---ttcgggga	383
B_anthraxis	390	cacgc-tcacctgttgattcgccaaatgcgcgattccacagctaacgttaa	438

SEQ175	384 ag---atcagaaccaccaatatccg---aacgaaa--aaggg-----	418
B_anthraxis	439 agtagctactgcacacccattggggcgtgtaacgttaagtcagggtcccttag	488
SEQ175	419 ttggcgg--catcgatgacgatcc-tttcgccaatgacggccagccgac	465
B_anthraxis	489 ttaaacgcaccacgaggataaacagattccatcaat--cgaaccac	531
SEQ175	466 gatattttcgtgatgattttgcggtt	492
B_anthraxis	532	531

```

# Program: needle
# Rundate: Mon Jul 31 07:15:58 2006
# Align_format: strepair
# Report_file: /ebi/extern/old-work/needle-20060731-0715585573420.output

```

```

#
# Aligned_sequences: 2
# 1: SEQ175
# 2: B_thuringiensis
# Matrix: ESLOS62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 556
# Identity: 238/556 (42.8%)
# Similarity: 238/556 (42.6%)
# Gaps: 98/556 (17.6%)
# Score: 1029.5
#
#=====

```

SEQ175	1	atgattaacgc-cgtcattttgtcggaaggttaacgagagatcc	44
B_thuringiens	1	ttagaacggttaaatcgtcgtcggaatctcgatcggttgac-ctacattt	49
SEQ175	45	ggaggttg---cgttacactcc---aagcggagtggtc---gttgccacg	84
B_thuringiens	50	gaaaatggatcgtcattctctgtaaatccagagtttcttggttacactg	99
SEQ175	85	tttacgc-----tcggcggtcaacc-----gtcc---gtttacaa	115
B_thuringiens	100	gttgcccggaattactagattgaccaaatgggttagagctttggttaccca	149
SEQ175	116	atcagcaggggcagcgggaaacggattttattcaatgtgtcgtttgcgc	165
B_thuringiens	150	aac--cagctcctgatggttgctgatataatgaaccagttgctccerac	197
SEQ175	166	cgcca-----ggcggaacacgtcgccaacttttgaanaaggggagctt	209
B_thuringiens	198	cgccattacggcggtcctaaaaattgtacgctttccgcaa-----gaactt	242
SEQ175	210	ggctgggtgtcgatggcgactgcaaaccccgagctatgaaatacaagag	259
B_thuringiens	243	--ctgttacatatacagcgttaccatcttgcctcctgtaattacagagtt	290
SEQ175	260	gtcgccgtgtgtacgtgacggnaagtggtggtgatagcgtccaaattctt	309
B_thuringiens	291	gaagcgtccatctacgcgtgctaaagctacccctttt---tcaataattt	337
SEQ175	310	gagccgaagggaacgagcagcagcagcagcagcagcagcagcagcagcagc	353
B_thuringiens	338	gctacgttttctgctgttttacgcatattac-acaattataaagtcag	386
SEQ175	354	ctactatggggatccattccattcgggcaagatcagaaccaccaattac	403
B_thuringiens	387	cttcac--ggtcacctgttgattcg-----caaatcgcgattcac	426

SEQ175	404	---ggaacgaaaaagggtttggccgcacgatgatgacgacgtcctttgcgcataa	451
R_thuringiens	427	agctaacgcttaaaag---tagctaacgc---aac-accatggggcgta	468
SEQ175	452	acg---gcacgcgatcgatgattt-----ctgatgatgatttgcgcgttt	492
R_thuringiens	469	acgtaaatgcag---ggtcctttagttaaagcaccacaggataaacacgatt	516
SEQ175	493		492
R_thuringiens	517	catcaa	522

```

# Program: needle
# Run date: Mon Jul 31 07:18:04 2006
# Align format: arspair
# Report file: /ebi/extern/old-work/needle_20060731-0718033686657.output

```

```

#
# Aligned sequences: 2
# 1: SEQ175
# 2: B_weihenstephensis
# Matrix: SELOSSUM62
# Gap penalty: 10.0
# Extend penalty: 0.5
#
# Length: 525
# Identity: 334/525 (63.6%)
# Similarity: 334/525 (63.6%)
# Gaps: 36/525 (6.9%)
# Score: 1725.0
#

```

```

SEQ175      1 atgattaaccgcgctcattttggtcggcagggttaacgagagacccgagtt      50
B_weihensteph 1 ttgatgaatcgtgttatcctcgttggtcgtttaactaaggaccctgactt      50

SEQ175      51 gcgttacactccaaagcgaggtggctgttgccacgtttacgtcgcggtca      100
B_weihensteph 51 acgttacacgcccgaatggtgttcagtagctactttttagctagctgtga      100

SEQ175      101 acgcctcgttttacaaatcagcagggcgagcgggaacggattttattcaa      150
B_weihensteph 101 atcgcgcaatttgcgaatcaacaaggtgagcgtgaagctgactttattaat      150

SEQ175      151 tctgtcgtttggcgccgcagcgagggaacacgtgcccaacttttggaaaaa      200
B_weihensteph 151 tctgtcaatatggcgtaaacagcagaaaacgtggcaattatttggaaaaa      200

SEQ175      201 ggggaagcttggctgggtgtcgtgacgtgacgggaagtggtggctgtagcgte      250
B_weihensteph 201 aggtagcttagcaggcgttagcaggacgtcttcaactcgttaattacgatg      250

SEQ175      251 atcaagaaggtcgcggtgtgtacgtgacgggaagtggtggctgtagcgte      300
B_weihensteph 251 gcaagaagtggtaaacgtgtatatgtacaagaagttcttcggcgagagcgt      300

SEQ175      301 caatttcttgagcgg---aaaggaaacgagcgagcagcgagg-----      338
B_weihensteph 301 caacttttagagccgcgtaatggcggtggggagcaacgtgggttcattcaa      350

SEQ175      339 --ggcga-cagcaggcgctactatggggatoca-----ttcccatte      378
B_weihensteph 351 tcaacaacccaatcagg-agctgggttcggtaaccaagctccaacccattc      399

SEQ175      379 gggcaagatc-agaaccaccaatatccgaacgaaaaaggggtttggcgca      427
B_weihensteph 400 ggtca--atctagtaattcaggtaaccaaggttaacagggaactccgga      447

```


SEQ175	428	t---cg---atgacgacccctttcgccaatgacggccagccgacgatat	470
B_weihensteph	445	tttacgaagaatgacacatccatttcgaatgttgggtcaaccgattgacat	497
SEQ175	471	ttctgatgatgatttgcggttt	492
B_weihensteph	498	ttcggacgacgatttaccattttaa	522

```
# Aligned_sequences: 2
# 1: SEQ175
# 2: B_subtilis
# Matrix: EBLOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5

# Length: 528
# Identity: 350/528 (66.3%)
# Similarity: 350/528 (66.3%)
# Gaps: 45/528 ( 8.5%)
# Score: 1860.0
```

SEQ175	1	atgattaaacccgctcatttggctgcgaggttaaacgagagatccggaatt	50
B_subtilis	1	atgcttaacgcgagttgtattatgctggaagactgcacaaaagaccagagct	50
SEQ175	51	gcgctacactccaaagcggagtggctgttgccacgtttacgtcgcgggtca	100
B_subtilis	51	tctgtatccgcgcaaaaggtgcggctgtgtctacgtttactcttgcgtgca	100
SEQ175	101	accgtccgttttacaacatcagcagggcgagcgggaaacggattttattcaa	150
B_subtilis	101	atcgtaacctatcagcaaccgtccggagaaactggaggcgatctcattaat	150
SEQ175	151	tgtgtcgtttggcgcgccagcgggaaacgcgcacactttttgaaaaa	200
B_subtilis	151	tgtgtaccttggagaagacaacgcgaaacactgtgcaaaactcttgaaaaa	200
SEQ175	201	ggggagcttggctggtgtcgatggccgactgcnaaacccgcagctatgaaa	250
B_subtilis	201	aggaagccttcagcgctagtatggccgtttacaacaacgaaactatgaaa	250
SEQ175	251	atcaagaagctcggcgtgtgtacgtacgcgaagtgtggtcgtatagcgtc	300
B_subtilis	251	accagcaaggacagcgtgtcttctgtacagaggtccaagctgnaagctgtt	300
SEQ175	301	caattttcttgagccagaaggaacg--agcg-----ag-----c	331
B_subtilis	301	caatttcttgagccgaaa--aacgcggcggtctctggttcaggtggatac	348
SEQ175	332	agcgaggg--gcgacagcagcgccg--tactatgg--gga-tccattc--	372
B_subtilis	349	aacgaaggaaacacagccg--ggagccagctactttgctggcggagccaaatg	397
SEQ175	373	-----caattcgggcagagatcagaaaccaccaatattccgaacgaaaaagg	417
B_subtilis	398	ataattccatttgggggaaatcaaaaacacacagagac--gcacatcagggq	444

SEQ175	418	tttggcgcacgcgatgcgcgacgtcttttgcgaatgacggccagcgcgcga	467
		.. .	
B_subtilis	445	---aacagctttaatgatgaacctttgccaacgacggccaacgcgattga	491
SEQ175	468	tatttctgatgatgatttgcggtt	492
		
B_subtilis	492	catctcggatgatgatcttcattctaa	519

[illegible]

[illegible]

```

# Program: needle
# RunDate: Mon Jul 31 07:22:20 2006
# Align_format: srsPair
# Report_file: /cbl/extserv/old-work/needle-20060731-07222012434590.output

```

```

# =====

```

```

# Aligned sequences: 2
# 1: SEQ175
# 2: B_clausii
# Matrix: ERIOSUM62
# Gap_penalty: 10.0
# Extend_penalty: 0.5
#
# Length: 552
# Identity: 257/552 (46.6%)
# Similarity: 257/552 (46.6%)
# Gaps: 126/552 (22.8%)
# Score: 1055.5
#

```

```

# =====

```

```

SEQ175      1      at-gattaacgcgctc----attttggctcg-gcaggttaacgaga      39
              || ||..||..||| |||...|| |..|...|||
B_clausii   1 Ttaaagtgaagatcatcgctcggaatatcaatcgaaacgctcattcgaga      50
SEQ175      40 gatccggaagttgcgtta-cactccaagcggagtgctgttgccacgcttta      88
              .||| || |||| ||..||..|||..|||...||| |||
B_clausii   51 ---acgg-gt--cgttatcatatccattagaacggctgcacaca-gttt--      92
SEQ175      89 cgtctcgcggtc--aacgcgtcgcttacaatcagcagggcgagcgg---g      133
              |..|| | |||| | |..|| |||| |..||..| .
B_clausii   93 -ggttgc--cagaacott--ggttgc---cagc--gcgctactgatca      130
SEQ175      134 aaacggattttattcaatgtgtgctttggcgccgccag--gcggaaaacg      181
              |||...||| |||...|| | |..||..|| | |....
B_clausii   131 aaaccaggattattccagag--gattggtttgactgttgcgaggt---      175
SEQ175      182 tcgcccactttttgaaaaggggagctt--ggctggtgtcgatggccgac      229
              |||..||..|| | |..|| | | |..||..|| |
B_clausii   176 tcgagaaatt-----ggacgctttcagc---aacgatttcgct-      210
SEQ175      230 tgcnaaccgcgcgct-----atgaaaatcagaaggtcggcgtgtgtac      273
              |..||..||..|| | |..|| | | |..||..|| |
B_clausii   211 tacaaaaacgcgctgccttcattattgtca--tagcttcgcttgccac      258
SEQ175      274 gtgacggaagt-ggtggtgatagcgtccaaattctctgagccgaaaggaa      322
              |||..|| |...|||..|| |..||..|| |..|...|
B_clausii   259 ---acggcgtcgactcctgcgaagctcctttttaaggaaattggcga      305
SEQ175      323 cgaagcg-agg-----agcgagggcgaca-----gcaggcggctact      358
              |..| | | |..||..|| | |..||..|| |
B_clausii   306 cgttctcagcgggtttgcgcgcagacacacagttaatgaagtgcagcttct      355
SEQ175      359 atgggggatocattcccatcggggcaagatcagaacc--accaatatar--c      404
              |..||..|| | |..||..|| | |..||..|| |
B_clausii   356 -----cgtctcctt--gctggtttgaaaacgagcgttgactgc      393

```



```

SEQ175      405 gaacgaaaaagggtttgggcgcgcgatcgatgacgat---cct--ttcgccaa      449
      .|.|||.|||.  |||||.|||.|||.|||.  |||.  |||||.
B_clausii  394 aagcgtaaaa---ttggctacagctacacogtttggcg'gaacgcgaat      439
      .|.|||.|||.|||.  |||.  |||.|||.|||.|||.|||.
SEQ175      450 tgacgggcacgcgat---cgatatttctgatgatgatttgcggtt      492
      .|.|||.|||.|||.  |||.  |||.|||.|||.|||.|||.
B_clausii  440 tcagggtracgcggttaagcg-----tcgcacaagaacaacacgggtttaa      484
      .|.|||.|||.|||.  |||.  |||.|||.|||.|||.|||.
SEQ175      493          492
B_clausii  485 aa      486

```

EXHIBIT 3

CLUSTAL W (1.8.3) multiple sequence alignment

Sequence format is Pearson
 Sequence 1: SEQ176 164 aa
 Sequence 2: G_kaustophilus 164 aa
 Start of Pairwise alignments
 Aligning...
 Sequences (1:2) Aligned, Score: 75
 Guide tree file created: [/ebi/extern/cluster-work/interactive/clusterw-20060731-05213563.dnd]
 Start of Multiple Alignment
 There are 1 groups
 Aligning...
 Group 1: Sequences: 2 Score:2667
 Alignment Score 773
 CLUSTAL-Alignment file created [/ebi/extern/clusterw-work/interactive/clusterw-20060731-05213563.aln]

```

SEQ176      MINRVILVCRITRDPELRYTFSGVAVATFTLAVNRPFNTQSYENQEGRRVYVTEVVADSV 60
G_kaustophilus MINRVILVCRITRDPELRYTFSGVAVATFTLAVNRPFNTQ----- 40
*****

SEQ176      QFLEPKGTSEQRGATAGGYQGGERETDFIQCVVWRQAEVANFLKKGSLAGVDCRLQTR 120
G_kaustophilus -----QGERETDFIQCVVWRQAEVANFLKKGSLAGVDCRLQTR 80
*****

SEQ176      -----GDPFFFGQDQNHQYFNEKGF 140
G_kaustophilus SYENQEGRRVYVTEVVADSVQFLEPKGTSEQRGATAGGYGDPFFFGQDQNHQYFNEKGF 140
*****

SEQ176      GRIDDDFFANDGQPIDISDDDLFF 164
G_kaustophilus GRIDDDFFANDGQPIDISDDDLFF 164
*****

```



```

Sequence format is Pearson
Sequence 1: SEQ176      161 aa
Sequence 2: E_anthraxis 176 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 56
Guide tree      file created: [/ebi/extern/clustalw-work/interactive/clustalw-
20060731-C5321442.dnd]
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences: 2      Score:2356
Alignment Score 337
CLUSTAL-Alignment file created [/ebi/extern/clustalw-work/interactive/clustalw-
20060731-05321442.aln]

```

[illegible]

```

Sequence format is Pearson
Sequence 1: SEQ176      164 aa
Sequence 2: B.thuringiensis 173 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 56
Guide tree      file created: [/ebi/extern/clusterw-work/interactive/clusterw-
20060731-05344058.dnd]
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences: 2      Score:2365
Alignment Score 351
CLUSTAL-Alignment file created [/ebi/extern/clusterw-work/interactive/clusterw-
20060731-05344058.ain]

```

[illegible]

CLUSTAL W (1.83) Multiple Sequence Alignments

```

Sequence format is Pearson
Sequence 1: SEQ176 164 aa
Sequence 2: B_weihenstephanensis 173 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 56
Guide tree file created: [/ebi/xtserv/clustalw-work/interactive/clustalw-
20060731-05393321.jnd]
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences: 2 Score:2361
Alignment Score 349
CLUSTAL-Alignment file created [/ebi/xtserv/clustalw-work/interactive/clustalw-
20060731-05393321.aln]

SEQ176 MINRVILVGRLLRDPFLRYTFSGVAVATFTLAVNRPFTNQSYENQEGRR--VYVTEVVAD 58
B_weihenstephanensis MNRVILVGRALTQDFOLRYTPNGVAVATFTLAVNPAFANQCGEREADFINCVIWRKQAE 60
*:*****:*:*****:*:*. *: . * : . :

SEQ176 SVCFLPEPKGTSEQRGATAGGYQGERETDFIQCVVWRQAEVAVFLKKGLAGVDC-- 115
B_weihenstephanensis VANYLKKGLSLAGVDGRLQTRNYDQ---DGRVYVTEVLAESVQ-FLEFRNGGGEQRGSF 116
.:*: . : * *: * : * . **.* **: . . :

SEQ176 RLQTRCDPF-----FFGQDQNHQYFNEKGFG--RIDDCFFANDCQPIDISDDDLPF 164
B_weihenstephanensis NQQPSGAGFGNQSNNFFGQSSNSGNQGNQGNSGFTKNDPFSNVGQPIDISDDDLPF 173
. *. " * ****.* .:*. :****:* *****

```

CLUSTAL W (1.82) Multiple Sequence Alignments

Sequence format is Pearson
 Sequence 1: SEQ176 164 aa
 Sequence 2: B_subtilis 172 aa
 Start of Pairwise alignments
 Aligning...
 Sequences (1:2) Aligned. Score: 59
 Guide tree file created: [/ebi/extern/clustalw-work/interactive/clustalw-20060731-05422505.dnd]
 Start of Multiple Alignment
 There are 1 groups
 Aligning...
 Group 1: Sequences: 2 Score:2492
 Alignment Score 388
 CLUSTAL-Alignment file created [/ebi/extern/clustalw-work/interactive/clustalw-20060731-05422505.aln]

```

SEQ176      MINRVILVGRLTROPELRYTPSGVAVATFTLAVNRFFTNOSYENQECRRVYVT--EVVAD 58
B_subtilis  MLNRVVLVGRLLTKDPELRYTPNGCAVATFTLAVNRFFTNOSGEREADFNCVTVRRQAEN 60
*:***:*****:*****:*.*****:*****:*.!. .  **  . . :

SEQ176      SVQFLPKGTISEQRGATAGGYOGERETDFIQCVVWRRQAENVANETKK-----GSL 110
B_subtilis  VANFLKKGLAGVDGRLQTRNYENQCCQ---RVFVTEVQAESVQFLPKNGGGSGSGGYN 117
.:**:. . :  *  *!:.:  :.*.***.*  :  *

SEQ176      AGVDGRLOTRG---DFFPFQDQNHQYPNEKGEGRIDDDPFANDGQPIDISDDDLFF 164
B_subtilis  EGNSSGGQYFGGGQDNPFEGGNONNORRNQC--NSFNDDPFANDGKPIDISDDDLFF 172
*.*. *  *  :  ***:***: *  . :*****:*****

```


CLUSTAL W (1.83) Multiple Sequence Alignments

```

Sequence format is Pearson
Sequence 1: SEQ176          164 aa
Sequence 2: B_licheniformis 170 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 60
Guide tree      file created:  [/ebi/extserv/clustalw-work/interactive/clustalw-
20060731-05435846.ndd]
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences:  2      Score:2430
Alignment Score 399
CLUSTAL-Alignment file created  [/ebi/extserv/clustalw-work/interactive/clustalw-
20060731-05435846.aln]

```

```

SEQ176          MINRVILVGRLTROPELAYTPSGVAVATFTLAVNRPFITNQSYENQEGRR--VYVTEVVD 58
B_licheniformis MINRVVLVGRLTROPELAYTPSGAAVATFTLAVNRFTITNQSGEREADFINCVVWRQAE 60
:***:*****:*****:*****:***:*.:.  *  .  .  :

SEQ176          SVQFLEPKGTSEQRGATAGGYQCERETDPIQCVVWRQAEVANFLAKGSLAGVDGRILQ 118
B_licheniformis VANFLKKGSLAGVDGRILQTRSYENQCGQ---RVYVTEVQAESVQFLEPKGGGSGSGYSG 117
.:**:.  .  :  *  :.:.  :  *  .  **.  *  :  **.  .  .  *

SEQ176          TRG-----DFFPFGQDQNHQYENKGFGRIDDDPFANDGQPIDISDDDLFF 164
B_licheniformis GQGGQHFGGGQNEPAPFGGSONHQRNQG--NSFNDDPFANDGKEIDISDDDLFF 170
:*  :  :  *  ***  .**:*  *  :  .  :*****:*****

```

CLUSTAL W (1.53) Multiple Sequence Alignments

```

Sequence format is Pearson
Sequence 1: SEQ176          164 aa
Sequence 2: B_halodurans    168 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 54
Guide tree      file created:  [/ebi/extserv/clustalw-work/interactive/clustalw-
20060731-05480066.dnd]
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1: Sequences:  2      Score:2356
Alignment Score 350
CLUSTAL-Alignment file created  [/ebi/extserv/clustalw-work/interactive/clustalw-
20060731-05480066.aln]

SEQ176      MYNRVILVGRLTRDFELRYTFSGVAVATFTLAVNRPFNTQSYENQEGRR-VYVTEVVADS 59
B_halodurans MLNRVVLVGRLTRDFELRYTFPGVAVANFTLAVNRPFNTQGGEREADFINCVVWRKQAE 60
*:***:*****:*****:***:*.:.      *.  *.

SEQ176      VQFLEPKGTSEQRGATAGGYQGERETDFIQCVVWRQAEN/VANFLKKGSLAGVDGRLQT 119
B_halodurans VANFLKKGS--LAGVDGRIQTRSYDNNEGRVFEVTEVMAESVQFLEPRGSGSQGGSNVDN 118
*      **:.  *.  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .
*      **:.  *.  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .

SEQ176      RG--DF-FPFGQDQNHQYFNEKG--FGRIDDDFFANDGQPIDISDDDLFF 164
B_halodurans FGGGSPNNFMGGNDFGQSGSGGRQSGGFSEDPFANDGKPIDISDDDLFF 168
*  .  *  *  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .  .

```

CLUSTAL W (1.83) Multiple Sequence Alignments

Sequence format is Pearson
 Sequence 1: SEQ176 164 aa
 Sequence 2: B_clausii 161 aa
 Start of Pairwise Alignments
 Aligning...
 Sequence (1:2) Aligned. Score: 54
 Guide tree file created: [/ebi/extern/cluster-work/interactive/cluster-
 20060731-05513189.dnd]
 Start of Multiple Alignment
 There are 1 groups
 Aligning...
 Group 1: Sequences: 2 Score: 2277
 Alignment Score 542
 CLUSTAL-Alignment file created [/ebi/extern/cluster-work/interactive/cluster-
 20060731-05513189.aln]

```

SEQ176      MINRVILVGRILTRDPFLRYTFSGVAVATFTLAVNRPFITNQSRYNCEGRVYVTEVVADS/ 60
B_clausii   MLNRVVLVGRILTRDPFLRFTPNGVAVANFTLAVNRPFISNQ----- 40
              *:::*****:*****:*****:

SEQ176      QFLEPKGTSEQRGATAGGYQGERETDFIQCVVWRQAEENVANFLKKSGLAGVDGRLOTR 120
B_clausii   -----QGEFEADFINCVVWRKPAENVANFLKKSGLAGVDGRVQTR 80
              *****:*****:*****:*****:

SEQ176      -----GDPFFPGQCDNRQYF---NEKGFGK----- 142
B_clausii   SYDNNRGRAVFVTEIVALSVOFLEPRNSQNSGNNPGFDQYGAGNQGSNGQYGGGSRNSG 140
              ... * : * * *: *.:

SEQ176      IDDDPFANDGQPIDISDDDLFF 164
B_clausii   YDNDPFSNDG-SIDISDDDLFF 161
              *:::***:*****

```